

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2000, 18:46:05 ; Search time 423.11 Seconds
(without alignments)
5830.493 Million cell updates/sec

Title: US-09-157-984-2

Perfect score: 399
Sequence: 1 aagggcaagactcttgcgca.....gccgcaactcatgagagcat 399

Scoring table: IDENTITY_MNC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
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38: gb_est38:*
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41: em_est40:*
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107: em_gss9:*
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109: em_gss11:*
110: em_gss12:*
111: gb_gss12:*
112: gb_gss13:*
113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:

```

Pred. NO. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description

LOCUS	BE098020	540 bp	mRNA	EST	12-JUN-2000
DEFINITION	UI-R-C4-anc-d-09-0-UI.s1 UI-R-C4 Rattus norvegicus cDNA clone				
ACCESSION	UI-R-C4-anc-d-09-0-UI 3', mRNA sequence.				
VERSION	BE098020				
KEYWORDS	BE098020.1	GI:8488914			
SOURCE	EST.				
ORGANISM	Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 540) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)				
JOURNAL	9704447.				
MEDLINE					
COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized spleen library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLY-A=yes.				
FEATURES	Location/Qualifiers				
source	1..540				
	/organism="Rattus norvegicus"				
	/strain="Sprague-Dawley"				
	/db_xref="taxon:10116"				
	/clone="UI-R-C4-anc-d-09-0-UI"				
	/clone_1lb="UI-R-C4"				
	/dev_stage="adult"				
	/lab_host="DH10B (Life Technologies)"				
	/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C4 library is a subtracted library of a series, ultimately derived from a mixture of tissues from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos. For a detailed description of the library from which this clone was derived, please visit our web site at rester.eng.uiowa.edu. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)				
	TAG_L1B=UI-R-C4				
	TAG_L1TSUB=spleen				
	TAG_SEQ=GAGAC				
BASE COUNT	129 a	122 c	135 g	154 t	
ORIGIN					
Query Match	23.8%	Score 94.8;	DB 33;	Length 540;	
Best Local Similarity	57.6%;	Pred. No. 2,3e-18;			
Matches 220; Conservative	0;	Mismatches 117;	Indels 45;	Gaps 1;	

	Query Match	22.4%	Score 89.4;	DB 35;	Length 639;	
	Best Local Similarity	56.3%	Pred. No. 1e-16;			
	Matches 220;	Conservative 0;	Mismatches 126;	Indels 45;	Gaps 1;	
OY	5 ccaacgacttttcgatcgccggagtagtactctgtgttgacagcgaagagcactggttg	64				
Dd	511 CCCATCCCATTTTCCACAGGGGCCGAATTCTCGGTGTGTGACAGTGTCAGCGGTGGGTGG	452				
OY	65 gcaacctgcaccacaagccacagacttacggyggcaatgaagtaacaggltgtccacattgttc	124				
Dd	451 GGGATAAGACACCGCCACACAGACATCAAGGGCAGAAGAGGTGATGGTGTGGAGAGTGTA	392				
OY	125 gcatacaaaacagtgtgtgaagaagcagatggtctctaagacacacagtygccgtgtgtgaagc	184				
Dd	391 ACATTAAACAPCAGTGTATTCAAACAGTACTTTTTTGAAGCACCAAGCCGGGACCCTAATC	332				
OY	185 ccatacggyggccccccaagccggtgtaagtagtcagcggyggttaagcaggaaccttaagct	244				
Dd	331 CCGTTGACACGG-----GGT	317				
OY	245 gtctgtggatcgacaagcagcactggaactcttatgtcaccaacgtgcacacacttgttc	304				
Dd	316 GCCGGGGCATGTAGCTCAAGACACGTGAACTCATATTGTAACACGACATCACACTTTGTCA	257				
OY	305 ggagcgttaactctctacaaaaccaagatgctcctgaggtcatccgaatcaacgcgctt	364				
Dd	256 AGGGGCTACCATGATGATGGACGAGCGGTGCCTGGCGGTTTATCCGATAGTAGGGGCT	197				
OY	365 gcgtgtgctctcctcagccgcaactcatgag	395				
Dd	196 GTGTGTGTGTGCTCAGCAGAGAGGCTGTGAG	166				
RESULT	3					
LOCUS	A1137043/c					
DEFINITION	UT-R-C2P-oj-c-01-0-UI.s1 UT-R-C2P Rattus norvegicus CDNA clone					
VERSION	A1137043					
KEYWORDS	A1137043.1 GI:3637820					
SOURCE	EST.					
ORGANISM	Norway rat. Rattus norvegicus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 436) Bonaldo,M.F., Lennon,G. and Soares,M.B.					
AUTHORS	Normalization and subtraction: two approaches to facilitate gene discovery					
TITLE	Genome Res. 6 (9), 791-806 (1996)					
JOURNAL	Contact: Soares, MB					
MEDLINE	97044477					
COMMENT	Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: mssoares@blue.weeg.uiowa.edu The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through the I.M.A.G.E. Consortium at LNL (infoimage.lnl.gov). IMAGE ID=1787550 The following repetitive elements were found in this CDNA sequence: I-61, >AT-rich<Low_complexity Seq primer: M13 Forward POLYA-No.					
FEATURES	Location/Qualifiers					
SOURCE	1..436 /organism="Rattus norvegicus" /strain="Sprague-Dawley"					

```

BASE COUNT
ORIGIN

106 a
93 c 108 g 129 t

/db_xref="taxon:10116"
/clone="UI-R-C2p-cf-c-01-0-01"
/clone_lib="UI-R-C2p"
/der_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' RSTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circle (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

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LOCUS	AW770784	512 bp	EST	04-MAY-2000
DEFINITION	h49g601.x1 NCI-CGAP Co17 Homo sapiens cDNA clone IMAGE:3026952 3'			
	similar to gb:X52599 BETA-NERVE GROWTH FACTOR PRECURSOR (HUMAN);,			
	mRNA sequence.			
ACCESSION	AW770784			
VERSION	AW770784.1	GI:7702831		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 512)			
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Robert Strausberg, Ph.D.			
	Tel.: (301) 496-1550			
	Email: Robert.Strausberg@nih.gov			
	Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.			
	Emmett-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies			
	, Inc. cDNA Library Arrayed by: Christa Frange, The I.M.A.G.E.			

Consortium DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: linfo@marie.llnl.gov
Seq primer: -400P from Gdbco
High quality sequence stop: 418.
Location/Qualifiers
1. 512
1. chr1:100000000-100000000

Query Match	Best Local Similarity	Score	GI	DB	Length
Matches 213; Conservative	55.5%;	Prod. No. 2,5e-11;	0; Mismatches 124;	Indels 47;	Gaps 2;
QY 12	ctcttcgcatcggcgagagtaactctgtgtgtgacagcgaagagacactggtgtgcaacct	71			
Db 499	CATCTTCACACAGGGGAAATTTCTCGTGTGTGACACAGTg--TCACGGTTGGGTGGGATAA	442			
QY 72	gaccacaagccacagactctacaggggacaaatgaatcaggtgtctgcacatgttgcacaa	131			
Db 441	GACCACCGCCACACACATCAAGGCAAGAGAGTATGTTGTGGCAGAGGTGAACATTTAA	382			
QY 132	caaatgtgtgtgagagagagatgtctctcagagacacagtcgcgtgtgtgcgaagcccatcg	191			
Db 381	CACACAGTATNTCAAAGATACCTTTTGTGTGAGACCAATGCCGGACCCAAATCCCGTTGA	322			
QY 192	ggcccccaagtcgggttcagaagagtcagcggcgttaaaacagaaacctctagctgtcgtg	251			
Db 321	CAGCG-----GGTCCCGGG 307				
QY 252	gatcgacaacagcagcagcagactcttatgtcaccacaagtgcacaccttgytgcggcgctt	311			
Db 306	CATGACCTCAAGACATGGAACATCATATTGACACACAGCATCACACCTTTGCAAGGGCGCT	247			
QY 312	aacgtctctacaaacacagattgctctgagaggttcatcagatcaaacgcgcttgcgtgtg	371			
Db 246	GACCATGTGATGCAAGCAGAGGCTGCTGCGGCTTTATCCGGATGATAGCGGCTGTGTGTG	187			
QY 372	ctctctcagcgcgcgaactcatgtgag 395				
Db 186	TGTCTCAGCAGGAAGGCTGTGTGAG 163				
RESULT 5	BE045524/c				
LOCUS	BE045524				
DEFINITION	hb23408.x1 NCI-GAP.Lu24 Homo sapiens cDNA clone IMAGE:2955926 3' similar to gb:452599 BETA-NERVE GROWTH FACTOR PRECURSOR (HUMAN);	EST	08-JUN-2000		
ACCESSION	BE045524				
VERSION	BE045524.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sap.:ens				
REFERENCE	Eukaryotic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/JNLN, send email to: info@image.linn.gov
seq primer: -40UP from Gibco.

FEATURES

BASE COUNT	113 a	104 c	107 g	118 t
ORIGIN				

RESULT	6
AI341450/c	
LOCUS	AI341450
DEFINITION	453 bp mRNA
ACCESSION	AI341450
VERSION	GI:4078377
KEYWORDS	EST
SOURCE	human.
ORGANISM	Homo sapiens

FEATURES

BASE COUNT	118 a	101 c	111 g	123 t
ORIGIN				

	Query Match	17.7%	Score 70.8	DB 10	Length 453
	Best Local Similarity	66.2%	Pred. No. 4.3e-11		
	Matches 102	Conservative 0	Mismatches 52	Indels 0	Gaps 0
QY	242	gctgctgctggtgagatcgacaacgagcacctgtgaaactcttatatgcaaccaacgtgcacaccttg	301		
Db	321	GGTGCCGGGGGCGGATTCGACCAAGGCACTGGAACTCATATTGTATGCCAGACAGTCCACACCTTGG	262		
QY	302	tgcggggcgcttaacgtctccacaaaaccccgatctgcttggaggttcatccgaalcaacgccg	361		
Db	261	TCAAGGCGCCTCAGCACCATGGATGGCAAGCAGAGGCGCTGGGGGCTTTATCCGAGATGATACGG	202		
QY	362	cttgctgtgtgcctctccacggccgcaactatggag	395		
Db	201	CCTGTGTGTGTGTGCTCTCAGCAGGAAGGCTGTGAG	168		

RESULT	7
LOCUS	AI700604/c
DEFINITION	AI700604. 442 bp mRNA EST 18-DEC-1999
ACCESSION	U00000.1 NC_000001 Homo sapiens CDNA IMAGE:2343379 3
VERSION	similar to gb:X52599 BETA-NERVE GROWTH FACTOR PRECURSOR (HUMAN);
KEYWORDS	mRNA sequence.
SOURCE	AI700604
ORGANISM	AI700604.1 GI:4988504
REFERENCE	EST.
AUTHORS	human.
TITLE	Homo sapiens
JOURNAL	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
	1 (bases 1 to 442)
	NCI-CCG http://www.ncbi.nlm.nih.gov/ncicgap.
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
	Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuquib, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP Clone Distribution Information can be found through the I.M.A.G.E. Consortium/BLNT at: www.bio.linn.gov/biopl/ncicgap/ncicgap.html
 Seq primer: -400P from GIBCO
 High quality sequence stop: 270.

FEATURES Location/Qualifiers
 1..416
 /organism="Homo sapiens"
 /db_xref="IMAGE:2580292"
 /clone_1db="NCI-CGAP_Ov32"
 /sex="female"
 /tissue="ovary"
 /note="Organ: ovary; Vector: PAMPI; mRNA made from ovarian carcinoma cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library."

BASE COUNT 105 a 91 c 118 t 6 others
ORIGIN
 Query Match 13.8%; Score 55.2; DB 19; Length 416;
 Best Local Similarity 60.4%; Pred. No. 2.3e-06;
 Matches 90; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 247 cctggagtcgacacgagcagctggaactctatgacacacgagcagcctgtgagc 306
DB 324 CGGGGCAATTGACAAACAGCACTGACATATGACACACGACCTGCTCAAG 265
QY 307 gcttaccgctccctcaaaacacagattcctggaggttcacacacacacgagcctg 366
DB 264 GCGGTGACCATGATGACAAACAGGCTGCGGCGTTATCCGATGATGATGACGCTGT 205
QY 367 gtgtgctcctcagccgcaactcatgag 395
DB 204 GTGTGTGTCTCAGCAGGAGGAGGCTGTGAG 176

RESULT 12 BE099666 562 bp mRNA EST 13-JUN-2000
LOCUS BE099666/c
DEFINITION UI-R-BJ1-atp-h-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
ACCESSION BE099666
VERSION BE099666.1 GI:8491545
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 562)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE Contact: Soares, MB
COMMENT Program for Rat Gene Discovery and Mapping
 University of Iowa

FEATURES Location/Qualifiers
 1..562
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone_1db="UI-R-BJ1-atp-h-09-0-UI"
 /clone_1db="UI-R-BJ1"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pRT3D-pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI. The UI-R-BJ1 library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 15 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library from which this clone was derived, please visit our web site at ratel.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_Lib=UI-R-BJ1
 TAG_Tissue=atrium at 16.5 dpc
 TAG_SEQ=GATTC

BASE COUNT 147 a 119 c 106 g 190 t
ORIGIN
 Query Match 13.6%; Score 54.2; DB 33; Length 562;
 Best Local Similarity 37.3%; Pred. No. 5.1e-06;
 Matches 98; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 19 catcgcgaggaactctctgtgtgacagcagcagcagcagcagcagcagcagcagc 78
DB 529 CACCGAGAGAGTACTAGTGTGAGAGTGAAGAGCTGTGGTACCCAGACTCTCA 470
QY 79 gccacagacttaccgagcagcagcagcagcagcagcagcagcagcagcagcagc 138
DB 469 GCCATTGACACTGGGACACACAGTTACAGTGTGGAGAGATCAAAACCGCAACTCT 410
QY 139 gtgaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 189
DB 409 CCTGTGATACATATTTTATGAAACAGAGGTGAAGAACCGCAGCAGTC 359

RESULT 13 AA995752 495 bp mRNA EST 13-APR-1999
LOCUS AA995752/c
DEFINITION c13c12 u1 NCI CGAP L45 Homo sapiens cDNA clone IMAGE:1605238 3'
 similar to gb:U52559 BETA-NERVE GROWTH FACTOR PRECURSOR (HUMAN);
 mRNA sequence.
ACCESSION AA995752
VERSION AA995752.1 GI:3182241
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 495)

TITLE The Wasyl-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine

```

FEATURES
  source
    This clone is available royalty-free through LNC ; contact the
    IMAGE Consortium (info@image.lnci.gov) for further information.
    Insert length: 707 Std Error: 0.00
    Seq primer: MOD.REGA+BT
    High quality sequence stop: 417.
    Location/Qualifiers
      1..455
        /organism="Homo sapiens"
        /db_xref="GDB:125556"
        /db_xref="taxon:9606"
        /clone="IMAGE:324054"

```

```

/clone_1lb="Soares_senescent_fibroblasts_NBHSP"
/issue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT773D (Pharmacia) with a modified
polylinker V-type: phagemid: Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - Oligo(dt)
primer 15',
TGTTCACAATCTGAGGTGGAGACGGCCCATTTTTTTTTTTTTTTT
3'},
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fátima Bonaldo."

```

Query Match	11.6%	Score 46.2	DB 40	Length 455
Best Local Similarity	60.1%	Pred. No. 0.0013		
Matches	92	Conservative	0	Mismatches 60; Indels 1; Gaps 1;
22Y	58	tggtgtgcgaactctaccacaagcccaagacttaacggcgcaatgaatgaatcaggtgtgcga	117	
22Y	220	ttgggtttgggggattatagaccacccgcccacacacatcacaaggcgcaagaggtgatgtgtttggga	279	
22Y	118	catgttcgcatacacaacggtgtgtgaagaagagatg-ctctacagagaccacgttcgcggt	176	
22Y	280	gaggatgaacatttaacaaacagctatttcaaaanaagtaactttttttgagaccacagtccttggga	339	
22Y	177	gtcgaagcccatcgtgggcccaccaagccgggtca	209	
22Y	340	cccaaatcccgtttgacagcngctnccggggcca	372	

RESULT 15
552484/c
DEFINITION
OCUS
552484
552484 463 bp mRNA
YD32403.s1 Stratagene fetal spleen (#937205) Homo sapiens CDNA
clone IMAGE:72869.3' similar to similar to db:X52599 BETA NERVE
GROWTH FACTOR PRECURSOR (HUMAN), mRNA sequence.
552484
552484.1 GI:654344
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisore,S., Dietrich,N., Dubuque,T., Faville,A., Gish,M., Hawkins
M., Hultman,M., Kucaba,T., Lacey,M., Le,N., Maddis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Mon Oct 30 10:20:14 2000

us-09-157-984-2.lst

Page 10

TITLE Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
JOURNAL Generation and analysis of 280,000 human expressed sequence tags
MEDLINE Genome Res. 6 (9), 807-828 (1996)
COMMENT 97044478

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 935
High quality sequence stops: 267 Source: IMAGE Consortium, LNL This
clone is available royalty-free through LNL; contact the IMAGE
Consortium (info@image.lnl.gov) for further information.
Insert length: 935 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 267.
Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"
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/clone_lib="Stratagene fetal spleen (#937205)"
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/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
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ECORI; Site: 2; XhoI; Cloned unidirectionally; Primer:
0.110 dt. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG
3' -3' adaptor sequence: 3' CTCGAGTCTTCTTTTCTTTT 3'";
5 others

BASE COUNT

113 a 104 c 111 g 130 t

ORIGIN

Query Match 11.4%; Score 45.4; DB 39; Length 463;
Best Local Similarity 68.1%; Pred No 0.0023;
Matches 92; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

Oy 263 agcacttggaactcttatgtcccaag-tgcacacctgtgagggcg-ttaagtccta 320
DB 297 AGCACTGGAACTCATATTGTACCCAGACTCACACCTTGTCAAGCGCTGACCATGGA 238
Oy 321 caaaagaacattgccttgagattcatcgaatcaagcgccgttcgtgtgcctcag 380
DB 237 TGGCAAGCAGAGCTCGCTCGCGTTATCCGATAGATACGCGCTGTGTGTGTCTCAG 178
Oy 381 ccgaactcatgag 395
DB 177 CAGGAGGCTGTGAG 163

Search completed: October 28, 2000, 20:30:08
Job time: 6243 sec